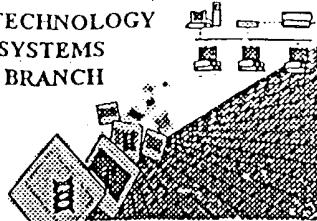# <u>RAW SEQUENCE LISTING</u>
<u>ERROR REPORT</u>

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/803,459_

Source: _1FWO_

Date Processed by STIC: _3/26/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u>
<u>VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<u>http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/803,459*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
                          prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
       Numbering   use **space characters**, instead.

4 ____ Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. **Please
                     ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                          each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
                          residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
       "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                        previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                        the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                        Artificial or Unknown sequences.**

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
       (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            This sequence is intentionally skipped

                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) ____ missing. **If intentional,** please insert the following lines for **each** skipped sequence.
       (NEW RULES)   <210> sequence id number
                            <400> sequence id number
                            000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
       (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                              In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
        Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                          is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                         Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                         "Unknown." Please explain source of genetic material in <220> to <223> section.
                         (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
        "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                         listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING   DATE: 03/26/2004
PATENT APPLICATION: US/10/803,459   TIME: 07:27:09

Input Set : D:\28758.txt
Output Set: N:\CRF4\03262004\J803459.raw

```
 3 <110> APPLICANT: Gertler, Arieh
 4         Krishna, Radha G.
 6 <120> TITLE OF INVENTION: LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO
 8 <130> FILE REFERENCE: 28758.1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/803,459
C--> 10 <141> CURRENT FILING DATE: 2004-03-19
10 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn version 3.2
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 630
16 <212> TYPE: DNA
17 <213> ORGANISM: human leptin receptor binding domain
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)..(630)
24 <220> FEATURE:
25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (6)..(6)
27 <223> OTHER INFORMATION: n is a, c, g, or t
29 <400> SEQUENCE: 1
30 atg gcn att gat gtc aat atc aat atc tca tgt gaa act gat ggg tac      48
31 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
32 1               5                   10                  15
34 tta act aaa atg act tgc aga tgg tca acc agt aca atc cag tca ctt      96
35 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
36             20                  25                  30
38 gcg gaa agc act ttg caa ttg agg tat cat agg agc agc ctt tac tgt     144
39 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
40         35                  40                  45
42 tct gat att cca tct att cat ccc ata tct gag ccc aaa gat tgc tat     192
43 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
44     50                  55                  60
46 ttg cag agt gat ggt ttt tat gaa tgc att ttc cag cca atc ttc cta     240
47 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
48 65                  70                  75                  80
50 tta tct ggc tac aca atg tgg att agg atc aat cac tct cta ggt tca     288
51 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
52                 85                  90                  95
54 ctt gac tct cca cca aca tgt gtc ctt cct gat tct gtg gtg aag cca     336
55 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
56             100                 105                 110
58 ctg cct cca tcc agt gtg aaa gca gaa att act ata aac att gga tta     384
59 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
```

Input Set : **D:\28758.txt**
Output Set: **N:\CRF4\03262004\J803459.raw**

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60        115              120              125
62 ttg aaa ata tct tgg gaa aag cca gtc ttt cca gag aat aac ctt caa    432
63 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
64    130              135              140
66 ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg    480
67 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
68 145              150              155              160
70 tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca    528
71 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
72              165              170              175
74 gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat    576
75 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
76          180              185              190
78 gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc    624
79 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
80          195              200              205
                                                                      630
82 atg gat
83 Met Asp
84       210

87 <210> SEQ ID NO: 2
88 <211> LENGTH: 210
89 <212> TYPE: PRT
90 <213> ORGANISM: human leptin receptor binding domain

92 <400> SEQUENCE: 2

94 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
95 1               5                   10                  15
98 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
99              20                  25                  30
102 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
103             35                  40                  45
106 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
107       50                  55                  60
110 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
111 65                  70                  75                  80
114 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
115                 85                  90                  95
118 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
119             100                 105                 110
122 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
123       115                 120                 125
126 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
127       130                 135                 140
130 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
131 145                 150                 155                 160
134 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
135             165                 170                 175
138 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
139             180                 185                 190
142 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
```

```
RAW SEQUENCE LISTING          DATE: 03/26/2004
PATENT APPLICATION:  US/10/803,459   TIME: 07:27:09

Input Set : D:\28758.txt
Output Set: N:\CRF4\03262004\J803459.raw
```

```
143            195              200              205
146 Met Asp
147      210
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 36
152 <212> TYPE: DNA
153 <213> ORGANISM: synthetic
155 <400> SEQUENCE: 3
156 ggaattccat atgattgatg tcaatatcaa tatctc                    36
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 39
161 <212> TYPE: DNA
162 <213> ORGANISM: synthetic
164 <400> SEQUENCE: 4
165 cataggaagc tttcaatcca tgacaactgt gtaggctgg                 39
168 <210> SEQ ID NO: 5
169 <211> LENGTH: 12
170 <212> TYPE: PRT
171 <213> ORGANISM: human leptin receptor fragment
174 <220> FEATURE:
175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (11)..(11)
177 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
179 <400> SEQUENCE: 5
181 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Xaa Glu
182 1               5                   10
185 <210> SEQ ID NO: 6
186 <211> LENGTH: 5
187 <212> TYPE: PRT
188 <213> ORGANISM: Consensus
191 <220> FEATURE:
192 <221> NAME/KEY: misc_feature
193 <222> LOCATION: (3)..(3)
194 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
196 <400> SEQUENCE: 6
198 Trp Ser Xaa Trp Ser
199 1               5
202 <210> SEQ ID NO: 7
203 <211> LENGTH: 627
204 <212> TYPE: DNA
205 <213> ORGANISM: chicken leptin receptor binding domain
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (1)..(627)
212 <220> FEATURE:
213 <221> NAME/KEY: misc_feature
214 <222> LOCATION: (6)..(6)
215 <223> OTHER INFORMATION: n is a, c, g, or t
217 <400> SEQUENCE: 7
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(handwritten annotations:) invalid <2137 response. See item 10 on Error Summary Sheet.

(handwritten:) invalid

(handwritten:) invalid

```
W--> 218  atg gcn gta gat gtg aat atc aat atc aaa tgt gaa act gat ggg tac      48
     219  Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
     220  1               5                   10                  15
     222  tta act aaa atg act tgc aga tgg tct gca aac cca aac gca ttg ctc      96
     223  Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
     224          20                  25                  30
     226  ttg ggg agt tcc ttg cag tta aga tac cac agg agc aaa att tat tgt     144
     227  Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
     228          35                  40                  45
     230  tct aac ttt cca agt act cct cca gaa tca gag gtg aaa gaa tgc cat     192
     231  Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
     232      50                  55                  60
     234  ttc cag agg aat cat tct tat gag tgc aca ttt cag cct gtt ttt ctt     240
     235  Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
     236  65                  70                  75                  80
     238  tta tct gga tat acc atg tgg att gag ctt aag cac tcg ctg gga aca     288
     239  Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
     240                  85                  90                  95
     242  ctt gaa tcc tca cca act tgt gtc gtt cca gca gat gtg gtg aag cca     336
     243  Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
     244              100                 105                 110
     246  ctg cct ccc tcc aac att aaa gca gag atc acc aga aac gat ggg ctg     384
     247  Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
     248          115                 120                 125
     250  ctg aac gtg agc tgg aca aac ccc gtg ttt aca aat gat gac ctt aag     432
     251  Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
     252      130                 135                 140
     254  ttt cag atc cgg tac gca gtg aac agg gaa gaa ctc aca tgg gag ctg     480
     255  Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
     256  145                 150                 155                 160
     258  tat gaa gtt cta agc gta cca aca aga tca gct gtg ata gaa gtg caa     528
     259  Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
     260                  165                 170                 175
     262  ctt tgt gtt gaa tat att gtt cag atc cgc tgc aga gcc ctg gat ggc     576
     263  Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
     264              180                 185                 190
     266  tta ggc tac tgg agc aac tgg agc aga tca gcc tat gca gct gta aaa     624
     267  Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
     268          195                 200                 205
     270  gat                                                                627
     271  Asp
     275  <210> SEQ ID NO: 8
     276  <211> LENGTH: 209
     277  <212> TYPE: PRT
     278  <213> ORGANISM: chicken leptin receptor binding domain
     280  <400> SEQUENCE: 8
     282  Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
     283  1               5                   10                  15
     286  Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
```

```
287             20                25                30
290 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
291         35                40                45
294 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
295     50                55                60
298 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
299 65                70                75                80
302 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
303             85                90                95
306 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
307         100               105               110
310 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
311         115               120               125
314 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
315     130               135               140
318 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
319 145               150               155               160
322 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
323             165               170               175
326 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
327             180               185               190
330 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
331         195               200               205
334 Asp
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/26/2004
PATENT APPLICATION: **US/10/803,459**   TIME: 07:27:10

Input Set : **D:\28758.txt**
Output Set: **N:\CRF4\03262004\J803459.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6
Seq#:5; Xaa Pos. 41
Seq#:6; Xaa Pos. 3
Seq#:7; N Pos. 6

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/803,459**

DATE: 03/26/2004
TIME: 07:27:10

Input Set : **D:\28758.txt**
Output Set: **N:\CRF4\03262004\J803459.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Current Application No
L:10  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
```